N1 End

filed July 11, 1989, now abandoned, all of which applications are hereby incorporated by reference herein in their entirety.

IN THE CLAIMS:

Please cancel claims 97 and 175 without prejudice.

Kindly substitute and add the following claims:

N2

39. (Five Times Amended) A kit for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said kit containing:

a first oligonucleotide comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT (SEQ ID NO: 22); and

a second oligonucleotide comprising the nucleotide base sequence of xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID NO: 2),

wherein x is nothing or is a sequence recognized by an RNA polymerase, and wherein each said oligonucleotide is from 22 to 100 bases in length.

N3

40. (Five Times Amended) An oligonucleotide for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said oligonucleotide being from 22 to 100 nucleotide bases in length and comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT (SEQ ID NO: 22) or a sequence of the same length and fully complementary thereto, wherein x is nothing or is a sequence recognized by an RNA polymerase.

41. (Six Times Amended) A kit for use in amplifying and detecting *Mycobacterium tuberculosis* nucleic acid, said kit containing:

a first oligonucleotide of from 24 to 100 nucleotide bases in length and comprising the nucleotide base sequence of SEQ ID NO: 3; and

a second oligonucleotide of from 22 to 100 nucleotide bases in length and comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT (SEQ ID NO: 22) or xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID NO: 2), wherein x is nothing or is a sequence recognized by an RNA polymerase.

42. (Six Times Amended) A kit for use in amplifying and detecting *Mycobacterium tuberculosis* nucleic acid, said kit containing:

a first oligonucleotide of from 23 to 100 nucleotide bases in length and comprising the nucleotide base sequence of SEQ ID NO: 8; and

a second oligonucleotide of from 20 to 100 nucleotide bases in length and comprising the nucleotide base sequence of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) or xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase.

N3 Cancel

49. (Four Times Amended) The kit of claim 48 further comprising a third oligonucleotide having a 3' end which is unmodified, wherein said third oligonucleotide is from 20 to 100 nucleotide bases in length and comprises the nucleotide base sequence of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) or xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase, and wherein the nucleotide base sequences of said second and third oligonucleotides are different.

N4

67. (Four Times Amended) A primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 22, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said primer oligonucleotide includes an at least 10 contiguous nucleotide base

N5

sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said region.

68. (Three Times Amended) The primer oligonucleotide of claim 67, said primer oligonucleotide being from 15 to 50 nucleotide bases in length.

69. (Three Times Amended) The primer oligonucleotide of claim 67, said primer oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 22 or a sequence of the same length and fully complementary thereto.

70. (Four Times Amended) The primer oligonucleotide of claim 67, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within the nucleotide base sequence of SEQ ID NO: 22 or a sequence of the same length and fully complementary thereto.

72. (Four Times Amended) The primer oligonucleotide of claim 71, said primer oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 1.

73. (Four Times Amended) The primer oligonucleotide of claim 71, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within the nucleotide base sequence of SEQ ID NO: 1.

---

75. (Four Times Amended) A composition for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said composition comprising:

a first primer oligonucleotide consisting of an oligonucleotide up to 100 nucleotide bases in length which hybridizes to a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base

sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO:23, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said first primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said first region; and

a second primer oligonucleotide consisting of an oligonucleotide up to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 7, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said second primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said second region.

N6 Cont

79. (Five Times Amended) The composition of claim 75 further comprising a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a third nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under reaction conditions, wherein the nucleotide base sequence of said third region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

N7

SUB 02

80. (Three Times Amended) The composition of claim 79, wherein said probe comprises the nucleotide base sequence of SEQ ID NO: 8 or a sequence of the same length and fully complementary thereto.

N8

84. (Four Times Amended) A composition for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said composition comprising first and second primer oligonucleotides, each of said primer oligonucleotides being up to 100 nucleotide bases in length,

wherein said first primer oligonucleotide hybridizes to a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, and wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 22, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said first primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said first region, and

wherein said second primer oligonucleotide hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, and wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 2, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said second primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said second region.

89. (Three Times Amended) The composition of claim 84 or 86 further comprising a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a third nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under reaction conditions, wherein the nucleotide base sequence of said third region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

N11 Sub B 04 90. (Twice Amended) The composition of claim 89, wherein said probe comprises the nucleotide base sequence of SEQ ID NO: 3 or a sequence of the same length and fully complementary thereto.

96. (Three Times Amended) A probe mix comprising:

N12 a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto; and

a helper oligonucleotide consisting essentially of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 9 and SEQ ID NO: 10.

98. (Twice Amended) A probe mix comprising:

N13 a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto; and

a helper oligonucleotide.

N14 100. (Four Times Amended) A kit for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said kit containing:

a first oligonucleotide comprising the nucleotide base sequence of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23); and

a second oligonucleotide comprising the nucleotide base sequence of xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7),

wherein x is nothing or is a sequence recognized by an RNA polymerase.

101. (Four Times Amended) A composition for use in detecting the presence of *Mycobacterium tuberculosis* in a sample, said composition comprising:

a) a hybridization probe of from 10 to 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3 and SEQ ID NO: 8, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto; and

b) a primer oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 2, SEQ ID NO: 7, SEQ ID NO: 22 and SEQ ID NO: 23, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto.

N14 cont

143. (Three Times Amended) An oligonucleotide for use in amplifying *Mycobacterium tuberculosis* nucleic acid, said oligonucleotide being from 20 to 100 nucleotide bases in length and comprising the nucleotide base sequence of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) or a sequence of the same length and fully complementary thereto, wherein x is nothing or a sequence recognized by an RNA polymerase.

N15

145. (Three Times Amended) A composition comprising:

N16

a first oligonucleotide having a 3' end which is not modified to reduce or block extension of said first oligonucleotide by a polymerase; and

a second oligonucleotide having a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase, wherein each of said first and second oligonucleotides comprises a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23), xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), and sequences of the same length and fully complementary thereto, wherein x is nothing or a sequence recognized by an RNA polymerase.

147. (Three Times Amended) A primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 23, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said region.

N17

N18

149. (Twice Amended) The primer oligonucleotide of claim 147, wherein said primer oligonucleotide is from 20 to 100 nucleotide bases in length.

150. (Twice Amended) The primer oligonucleotide of claim 69, wherein said primer oligonucleotide is from 22 to 100 nucleotide bases in length.

151. (Three Times Amended) The primer oligonucleotide of claim 147, wherein said primer oligonucleotide comprises the nucleotide base sequence of SEQ ID NO: 23 or a sequence of the same length and fully complementary thereto.

152. (Three Times Amended) The primer oligonucleotide of claim 147, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within the nucleotide base sequence of SEQ ID NO: 23 or a sequence of the same length and fully complementary thereto.

157. (Twice Amended) The composition of claim 101 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 9 and SEQ ID NO: 10, and sequences of the same length and fully complementary thereto.

158. (Twice Amended) A kit comprising a primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 22 and SEQ ID NO: 23, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto, and wherein said oligonucleotide primer includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said region.

159. (Twice Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under reaction conditions between a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, or a sequence of the same length and fully complementary thereto, and a hybridization probe of from 10 to 100 nucleotide bases in length comprising a

nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of said region, or a sequence of the same length and fully complementary thereto, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

160. (Twice Amended) A composition for use in detecting the presence of *Mycobacterium tuberculosis* in a sample, said composition comprising:

a) a hybridization probe of from 10 to 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto; and

b) a primer oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting the nucleotide base sequences of SEQ ID NO: 22 and SEQ ID NO: 2, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto.

161. (Twice Amended) The composition of claim 160 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 4 and SEQ ID NO: 5, and sequences of the same length and fully complementary thereto.

162. (Twice Amended) A kit comprising a primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 22, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said first region.

163. (Twice Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under reaction conditions between a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, or a sequence of the same length and fully complementary thereto, and a hybridization probe of from 10 to 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of said region, or a sequence of the same length and fully complementary thereto, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

164. (Twice Amended) A composition for use in detecting the presence of *Mycobacterium tuberculosis* in a sample, said composition comprising:

a) a hybridization probe of from 10 to 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a first nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said first region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto; and

b) a primer oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 23 and SEQ ID NO: 7, the RNA equivalents thereof, and sequences of the same length and fully complementary thereto.

165. (Twice Amended) The composition of claim 164 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting the nucleotide base sequences of SEQ ID NO: 9 and SEQ ID NO: 10, and sequences of the same length and fully complementary thereto.

166. (Twice Amended) A kit comprising a primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 23, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said region.

167. (Twice Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under reaction conditions between a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, or a sequence of the same length and fully complementary thereto, and a hybridization probe at least 10 nucleotide bases in length, wherein the entire nucleotide base sequence of said probe hybridizes with specificity to said region, or the sequence perfectly complementary thereto, and wherein the nucleotide base sequence of said region is selected from the

N19

group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

168. (Twice Amended) The kit of claim 41 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 4 and SEQ ID NO: 5, and sequences of the same length and fully complementary thereto.

169. (Twice Amended) The kit of claim 42 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 9 and SEQ ID NO: 10, and sequences of the same length and fully complementary thereto.

N19 Cancel

173. (Amended) The kit of claim 162 further comprising a second primer oligonucleotide up to 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 2, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto, and wherein said second primer oligonucleotide includes an at least 10 contiguous nucleotide base sequence which is fully complementary to an at least 10 contiguous nucleotide base sequence contained within said second region.

N20

174. (Amended) The kit of claim 166, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 23 or a sequence of the same length and fully complementary thereto.

176. (Amended) A hybridization probe of from 10 to 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 3, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

N21

177. (Amended) A hybridization probe at least 10 nucleotide bases in length, wherein the entire nucleotide base sequence of said probe hybridizes with specificity to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of the nucleotide base sequences of SEQ ID NO: 8, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

178. (New) An oligonucleotide at least 20 bases in length, wherein the nucleotide base sequence of said oligonucleotide consists of or is contained within the nucleotide base sequence xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7) or a sequence of the same length and fully complementary thereto, wherein x is nothing or a sequence recognized by an RNA polymerase.

N22

179. (New) A kit comprising a primer oligonucleotide at least 10 nucleotide bases in length, wherein the entire nucleotide base sequence of said primer hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group of nucleotide base sequences of SEQ ID NO: 7, the RNA equivalent thereof, and sequences of the same length and fully complementary thereto.

* * * * *